

**Vir box sequences in *Agrobacterium tumefaciens* pTiC58 and A6**

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The consensus Vir box sequence (TNCAATTGAAAPy) is located in the upstream region of the six vir region operons in the octopine plasmid pTiA6 (1). Examination of the upstream vir region sequences from the nopaline plasmid pTiC58 (2,3,4,5,6) reveals that Vir box sequences are located 117-163 bps upstream of the first ORF in five of the six vir region operons. The lack of a Vir box upstream of the nopaline virG is consistent with the large DNA rearrangements observed upstream of the nopaline virG (2) operon when compared to the octopine operon, and with the lack of inducibility of the nopaline virG (7) when compared to the octopine virG operon (8).

<u>Operon</u>	<u>Sequence</u> <u>pTiA6</u>	<u>Position</u>	<u>Homology</u>	<u>Sequence</u> <u>pTiC58</u>	<u>Position</u>	<u>Homology</u>
<u>virA</u>	TTCACTTGAAAC	-115	10/11	TTCATTGAAAC	-117	11/11
<u>virB</u>	TTCAATTGAAAT	-130	11/11	TTCAAATGAAAT	-132	10/11
	AGCAATTGAAAA	-110	9/11			
<u>virC</u>	TATAATTGCTAC	-147	8/11	TACAATTGAAAT	-139	11/11
	TACAATTGCAAT	-138	10/11	TACAATAAAATT	-122	7/11
	TTTAATTATAAC	-127	8/11	TAAAATTGAAAT	-117	10/11
	CGAATTGAAAT	-116	8/11			
<u>virG</u>	TTCACTGTAAAC	-111	9/11	NOT FOUND		
	AACGATTGAGAA	-99	7/11			
	TAAAATTGAAAT	-78	10/11			
<u>virD</u>	TTAAATTGCAAT	-151	9/11	TTCAATTTTATT	-163	7/11
	TGCAATTGTAGC	-145	9/11	TTTTATTGTAAT	-158	7/11
	AGCAATTATATT	-136	10/11	TATAATTTCAT	-147	8/11
				TTCAATTGTAAT	-141	10/11
<u>virE</u>	TGCAGTTGAAAC	-258	9/11	TACATATGAAAC	-126	9/11
				TGCATTGAAAG	+1716	9/11

**Position:** Distance of first base in Vir box sequence to ATG initiation codon in first ORF of operon.

**Homology:** Number of bases homologous to Vir box / total number of specific bases in Vir box sequence.

**Note:** pTiA6 virE ORF#1 is analogous to pTiC58 virE ORF#2. The virB operon of pTiC58 has not been completely sequenced.

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